



PCT

RAW SEQUENCE LISTING

DATE: 10/06/2004

PATENT APPLICATION: US/10/509,558

TIME: 16:00:46

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10062004\J509558.raw

5 <110> APPLICANT: The Genetics Company
 9 <120> TITLE OF INVENTION: Growth Regulating Proteins
 13 <130> FILE REFERENCE: 06259PC
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/509,558
 C--> 17 <141> CURRENT FILING DATE: 2004-09-24
 17 <160> NUMBER OF SEQ ID NOS: 5
 21 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 27 <211> LENGTH: 2096
 29 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 39 <222> LOCATION: (76)..(1950)
 41 <223> OTHER INFORMATION:
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 46 ggcacgagggc ggaagtgttc cggggtccgt ggggagcagg agagggagggc ggcggaccgt 60
 48 cccgcgcggg gcacg atg ttg aac atg tgg aag gtg cgc gag ctg gtg gac 111
 49 Met Leu Asn Met Trp Lys Val Arg Glu Leu Val Asp
 50 1 5 10
 52 aaa gcc acc aat gtt gtt atg aat tat tca gag atc gag tct aag gtt 159
 53 Lys Ala Thr Asn Val Val Met Asn Tyr Ser Glu Ile Glu Ser Lys Val
 55 15 20 25
 57 cga gag gca acg aac gat gat cct tgg gga cct tct ggg caa ctc atg 207
 58 Arg Glu Ala Thr Asn Asp Asp Pro Trp Gly Pro Ser Gly Gln Leu Met
 59 30 35 40
 61 gga gag att gcc aag gct aca ttt atg tat gaa caa ttt cca gaa ctt 255
 62 Gly Glu Ile Ala Lys Ala Thr Phe Met Tyr Glu Gln Phe Pro Glu Leu
 63 45 50 55 60
 65 atg aac atg ctt tgg tca cga atg tta aaa gac aac aaa aag aat tgg 303
 66 Met Asn Met Leu Trp Ser Arg Met Leu Lys Asp Asn Lys Lys Asn Trp
 67 65 70 75
 69 aga aga gtt tat aag tcg ttg ctg ctc cta gct tac ctc ata agg aat 351
 70 Arg Arg Val Tyr Lys Ser Leu Leu Leu Leu Ala Tyr Leu Ile Arg Asn
 71 80 85 90
 73 gga tca gag cgt gtt gtt aca agt gcc aga gaa cac att tat gat tta 399
 74 Gly Ser Glu Arg Val Val Thr Ser Ala Arg Glu His Ile Tyr Asp Leu
 75 95 100 105
 77 cga tcc ctg gaa aat tac cac ttt gta gat gag cat ggt aag gat caa 447
 78 Arg Ser Leu Glu Asn Tyr His Phe Val Asp Glu His Gly Lys Asp Gln
 79 110 115 120
 81 ggt ata aat att cga cag aag gtg aag gaa ttg gtt gaa ttt gcc cag 495
 82 Gly Ile Asn Ile Arg Gln Lys Val Lys Glu Leu Val Glu Phe Ala Gln

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83	125	130	135	140	
85	gat gac gac agg ctt cgt gaa gag cga aag aaa gca aag aag aac aaa				543
86	Asp Asp Asp Arg Leu Arg Glu Glu Arg Lys Lys Ala Lys Lys Asn Lys				
88	145	150	155		
90	gac aag tat gtt ggg gtt tcc tca gac agt gtt gga gga ttc aga tac				591
91	Asp Lys Tyr Val Gly Val Ser Ser Asp Ser Val Gly Gly Phe Arg Tyr				
92	160	165	170		
94	agt gaa aga tat gat cct gag ccc aaa tca aaa tgg gat gag gag tgg				639
95	Ser Glu Arg Tyr Asp Pro Glu Pro Lys Ser Lys Trp Asp Glu Glu Trp				
96	175	180	185		
98	gat aaa aac aag agt gct ttt cca ttc agt gat aaa tta ggt gag ctg				687
99	Asp Lys Asn Lys Ser Ala Phe Pro Phe Ser Asp Lys Leu Gly Glu Leu				
100	190	195	200		
102	agt gat aaa att gga agc aca att gat gac acc atc agc aag ttc cgg				735
103	Ser Asp Lys Ile Gly Ser Thr Ile Asp Asp Thr Ile Ser Lys Phe Arg				
104	205	210	215	220	
106	agg aaa gat aga gaa gac tct cca gaa aga tgc agc gac agc gat gag				783
107	Arg Lys Asp Arg Glu Asp Ser Pro Glu Arg Cys Ser Asp Ser Asp Glu				
108	225	230	235		
110	gaa aag aaa gcg aga aga ggc aga tct ccc aaa ggt gaa ttc aaa gat				831
111	Glu Lys Lys Ala Arg Arg Gly Arg Ser Pro Lys Gly Glu Phe Lys Asp				
112	240	245	250		
114	gaa gag gag act gtg acg aca aag cat att cat atc aca cag gcc aca				879
115	Glu Glu Glu Thr Val Thr Thr Lys His Ile His Ile Thr Gln Ala Thr				
116	255	260	265		
118	gag acc acc aca acc aga cac aag cgc aca gca aat cct tcc aaa acc				927
119	Glu Thr Thr Thr Thr Arg His Lys Arg Thr Ala Asn Pro Ser Lys Thr				
121	270	275	280		
123	att gat ctt gga gca gca gca cat tac aca ggg gac aaa gca agt cca				975
124	Ile Asp Leu Gly Ala Ala Ala His Tyr Thr Gly Asp Lys Ala Ser Pro				
125	285	290	295	300	
127	gat cag aat gct tca acc cac aca cct cag tct tca gtt aag act tca				1023
128	Asp Gln Asn Ala Ser Thr His Thr Pro Gln Ser Ser Val Lys Thr Ser				
129	305	310	315		
131	gtg cct agc agc aag tca tct ggt gac ctt gtt gat ctg ttt gat ggc				1071
132	Val Pro Ser Ser Lys Ser Ser Gly Asp Leu Val Asp Leu Phe Asp Gly				
133	320	325	330		
135	acc agc cag tca aca gga gga tca gct gat tta ttc gga gga ttt gct				1119
136	Thr Ser Gln Ser Thr Gly Gly Ser Ala Asp Leu Phe Gly Gly Phe Ala				
137	335	340	345		
139	gac ttt ggc tca gct gct gca tca ggc agt ttc cct tcc caa gta aca				1167
140	Asp Phe Gly Ser Ala Ala Ala Ser Gly Ser Phe Pro Ser Gln Val Thr				
141	350	355	360		
143	gca aca agt ggg aat gga gac ttt ggt gac tgg agt gcc ttc aac caa				1215
144	Ala Thr Ser Gly Asn Gly Asp Phe Gly Asp Trp Ser Ala Phe Asn Gln				
145	365	370	375	380	
147	gcc cca tca ggc cct gtt gct tcc agt ggc gag ttc ttt ggc agt gcc				1263
148	Ala Pro Ser Gly Pro Val Ala Ser Ser Gly Glu Phe Phe Gly Ser Ala				
149	385	390	395		

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151 tca cag cca gcg gta gaa ctt gtt agt ggc tca caa tca gct cta ggc      1311
152 Ser Gln Pro Ala Val Glu Leu Val Ser Gly Ser Gln Ser Ala Leu Gly
154      400      405      410
156 cca cct cct gct gcc tca aat tct tca gac ctg ttt gat ctt atg ggc      1359
157 Pro Pro Pro Ala Ala Ser Asn Ser Ser Asp Leu Phe Asp Leu Met Gly
158      415      420      425
160 tcg tcc cag gca acc atg aca tct tcc cag agt atg aat ttc tct atg      1407
161 Ser Ser Gln Ala Thr Met Thr Ser Ser Gln Ser Met Asn Phe Ser Met
162      430      435      440
164 atg agc act aac act gtg gga ctt ggt ttg cct atg tca aga tca cag      1455
165 Met Ser Thr Asn Thr Val Gly Leu Gly Leu Pro Met Ser Arg Ser Gln
166 445      450      455      460
168 aat aca gat atg gtc cag aaa tca gtc agc aaa acc ttg ccc tct act      1503
169 Asn Thr Asp Met Val Gln Lys Ser Val Ser Lys Thr Leu Pro Ser Thr
170      465      470      475
172 tgg tct gac ccc agt gta aac atc agc cta gac aac tta cta cct ggt      1551
173 Trp Ser Asp Pro Ser Val Asn Ile Ser Leu Asp Asn Leu Leu Pro Gly
174      480      485      490
176 atg cag cct tcc aaa ccc cag cag cca tca ctg aat aca atg att cag      1599
177 Met Gln Pro Ser Lys Pro Gln Gln Pro Ser Leu Asn Thr Met Ile Gln
178      495      500      505
180 caa cag aat atg cag cag cct atg aat gtg atg act caa agt ttt gga      1647
181 Gln Gln Asn Met Gln Gln Pro Met Asn Val Met Thr Gln Ser Phe Gly
182      510      515      520
184 gct gtg aac ctc agt tct cca tcg aac atg ctt cct gtc cgg ccc caa      1695
185 Ala Val Asn Leu Ser Ser Pro Ser Asn Met Leu Pro Val Arg Pro Gln
187 525      530      535      540
189 act aat gct ttg ata ggg gga ccc atg cct atg agc atg ccc aat gtg      1743
190 Thr Asn Ala Leu Ile Gly Gly Pro Met Pro Met Ser Met Pro Asn Val
191      545      550      555
193 atg act ggc acc atg gga atg gcc cct ctt gga aat act ccg atg atg      1791
194 Met Thr Gly Thr Met Gly Met Ala Pro Leu Gly Asn Thr Pro Met Met
195      560      565      570
197 aac cag agc atg atg ggc atg aac atg aac ata ggg atg tcc gct gct      1839
198 Asn Gln Ser Met Met Gly Met Asn Met Asn Ile Gly Met Ser Ala Ala
199      575      580      585
201 ggg atg ggc ttg aca ggc aca atg gga atg ggc atg ccc aac ata gcc      1887
202 Gly Met Gly Leu Thr Gly Thr Met Gly Met Gly Met Pro Asn Ile Ala
203      590      595      600
205 atg act tct gga act gtg caa ccc aag caa gat gcc ttt gca aat ttc      1935
206 Met Thr Ser Gly Thr Val Gln Pro Lys Gln Asp Ala Phe Ala Asn Phe
207 605      610      615      620
209 gcc aat ttt agc aaa taagagattg taaaagaagc agattgaatg aagaattttt      1990
210 Ala Asn Phe Ser Lys
211      625
213 agctgtgcag ataggtgatg ttgggatgga aaatgctaata caactaccct ttctttttatc      2050
215 aagtaattaa aataaatcta cataaaaaaa aaaaaaaaaa aaaaaa      2096
218 <210> SEQ ID NO: 2
220 <211> LENGTH: 625

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222 <212> TYPE: PRT
224 <213> ORGANISM: Homo sapiens
228 <400> SEQUENCE: 2
230 Met Leu Asn Met Trp Lys Val Arg Glu Leu Val Asp Lys Ala Thr Asn
231 1 5 10 15
234 Val Val Met Asn Tyr Ser Glu Ile Glu Ser Lys Val Arg Glu Ala Thr
235 20 25 30
238 Asn Asp Asp Pro Trp Gly Pro Ser Gly Gln Leu Met Gly Glu Ile Ala
239 35 40 45
242 Lys Ala Thr Phe Met Tyr Glu Gln Phe Pro Glu Leu Met Asn Met Leu
243 50 55 60
246 Trp Ser Arg Met Leu Lys Asp Asn Lys Lys Asn Trp Arg Arg Val Tyr
247 65 70 75 80
250 Lys Ser Leu Leu Leu Ala Tyr Leu Ile Arg Asn Gly Ser Glu Arg
251 85 90 95
254 Val Val Thr Ser Ala Arg Glu His Ile Tyr Asp Leu Arg Ser Leu Glu
255 100 105 110
258 Asn Tyr His Phe Val Asp Glu His Gly Lys Asp Gln Gly Ile Asn Ile
259 115 120 125
262 Arg Gln Lys Val Lys Glu Leu Val Glu Phe Ala Gln Asp Asp Asp Arg
263 130 135 140
266 Leu Arg Glu Glu Arg Lys Lys Ala Lys Lys Asn Lys Asp Lys Tyr Val
267 145 150 155 160
270 Gly Val Ser Ser Asp Ser Val Gly Gly Phe Arg Tyr Ser Glu Arg Tyr
271 165 170 175
274 Asp Pro Glu Pro Lys Ser Lys Trp Asp Glu Glu Trp Asp Lys Asn Lys
275 180 185 190
278 Ser Ala Phe Pro Phe Ser Asp Lys Leu Gly Glu Leu Ser Asp Lys Ile
279 195 200 205
282 Gly Ser Thr Ile Asp Asp Thr Ile Ser Lys Phe Arg Arg Lys Asp Arg
283 210 215 220
286 Glu Asp Ser Pro Glu Arg Cys Ser Asp Ser Asp Glu Glu Lys Lys Ala
287 225 230 235 240
290 Arg Arg Gly Arg Ser Pro Lys Gly Glu Phe Lys Asp Glu Glu Glu Thr
291 245 250 255
294 Val Thr Thr Lys His Ile His Ile Thr Gln Ala Thr Glu Thr Thr Thr
295 260 265 270
298 Thr Arg His Lys Arg Thr Ala Asn Pro Ser Lys Thr Ile Asp Leu Gly
299 275 280 285
303 Ala Ala Ala His Tyr Thr Gly Asp Lys Ala Ser Pro Asp Gln Asn Ala
304 290 295 300
307 Ser Thr His Thr Pro Gln Ser Ser Val Lys Thr Ser Val Pro Ser Ser
308 305 310 315 320
311 Lys Ser Ser Gly Asp Leu Val Asp Leu Phe Asp Gly Thr Ser Gln Ser
312 325 330 335
315 Thr Gly Gly Ser Ala Asp Leu Phe Gly Gly Phe Ala Asp Phe Gly Ser
316 340 345 350
319 Ala Ala Ala Ser Gly Ser Phe Pro Ser Gln Val Thr Ala Thr Ser Gly
320 355 360 365

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323 Asn Gly Asp Phe Gly Asp Trp Ser Ala Phe Asn Gln Ala Pro Ser Gly
324      370      375      380
327 Pro Val Ala Ser Ser Gly Glu Phe Phe Gly Ser Ala Ser Gln Pro Ala
328 385      390      395      400
331 Val Glu Leu Val Ser Gly Ser Gln Ser Ala Leu Gly Pro Pro Pro Ala
332      405      410      415
335 Ala Ser Asn Ser Ser Asp Leu Phe Asp Leu Met Gly Ser Ser Gln Ala
336      420      425      430
339 Thr Met Thr Ser Ser Gln Ser Met Asn Phe Ser Met Met Ser Thr Asn
340      435      440      445
343 Thr Val Gly Leu Gly Leu Pro Met Ser Arg Ser Gln Asn Thr Asp Met
344      450      455      460
347 Val Gln Lys Ser Val Ser Lys Thr Leu Pro Ser Thr Trp Ser Asp Pro
348 465      470      475      480
351 Ser Val Asn Ile Ser Leu Asp Asn Leu Leu Pro Gly Met Gln Pro Ser
352      485      490      495
355 Lys Pro Gln Gln Pro Ser Leu Asn Thr Met Ile Gln Gln Gln Asn Met
356      500      505      510
359 Gln Gln Pro Met Asn Val Met Thr Gln Ser Phe Gly Ala Val Asn Leu
360      515      520      525
363 Ser Ser Pro Ser Asn Met Leu Pro Val Arg Pro Gln Thr Asn Ala Leu
364      530      535      540
367 Ile Gly Gly Pro Met Pro Met Ser Met Pro Asn Val Met Thr Gly Thr
368 545      550      555      560
371 Met Gly Met Ala Pro Leu Gly Asn Thr Pro Met Met Asn Gln Ser Met
372      565      570      575
375 Met Gly Met Asn Met Asn Ile Gly Met Ser Ala Ala Gly Met Gly Leu
376      580      585      590
379 Thr Gly Thr Met Gly Met Gly Met Pro Asn Ile Ala Met Thr Ser Gly
380      595      600      605
383 Thr Val Gln Pro Lys Gln Asp Ala Phe Ala Asn Phe Ala Asn Phe Ser
384      610      615      620
387 Lys
388 625

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391 <210> SEQ ID NO: 3

393 <211> LENGTH: 2705

395 <212> TYPE: DNA

397 <213> ORGANISM: Drosophila melanogaster

401 <220> FEATURE:

403 <221> NAME/KEY: CDS

405 <222> LOCATION: (262)..(2208)

407 <223> OTHER INFORMATION:

W--> 411 <400> 3

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414 tttttacatt tttgtttgcg gaaagcgcggt gtgcgagaca ggtgcgccgt ttccatgcaa 120
416 aagtgc aaat cgtcagctgc aaaacagtca gaaaacggca cgccaagcga aaacgagttc 180
418 gacgtcttgt tgtagttgga ttttccagcc acttttgcgac gagattgtgt gaaaaattcc 240
420 gtagcattca atagtctcaa a atg gtg gat aaa ttc atc agc atg tgg aaa 291
421      Met Val Asp Lys Phe Ile Ser Met Trp Lys

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VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10062004\J509558.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:45 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:41

L:411 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:407